SEQUENCE LISTING

<110> Iruela-Arispe, Luisa
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Fronwald, James A.
Terrett, Jonathan A.

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Pro Thr Leu Leu Leu Leu Ala Ala Ala Leu Leu Ala Val Ser Asp Ala
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ctc ggg cgc ccc tcc gag gag gac gag gag cta gtg gtg ccg gag ctg   144
Leu Gly Arg Pro Ser Glu Glu Asp Glu Glu Leu Val Val Pro Glu Leu
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gag cgc gcc ccg gga cac ggg acc acg cgc ctc cgc ctg cac gcc ttt   192
Glu Arg Ala Pro Gly His Gly Thr Thr Arg Leu Arg Leu His Ala Phe
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 65                  70                  75                  80

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ccg ctt ccg gaa acc gac ctg gcg cac tgc ttc tac tcc ggc acc gtg   336
Pro Leu Pro Glu Thr Asp Leu Ala His Cys Phe Tyr Ser Gly Thr Val
            100                 105                 110

aat ggc gat ccc agc tcg gct gcc gcc ctc agc ctc tgc gag ggc gtg   384
Asn Gly Asp Pro Ser Ser Ala Ala Ala Leu Ser Leu Cys Glu Gly Val
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gta ggc ggc acg tgc ggg gtc gtg gac gac gag ccc cgg ccg act ggg 576
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180 185 190

aaa gcg gag acc gaa gac gag gac gaa ggg act gag ggc gag gac gaa 624
Lys Ala Glu Thr Glu Asp Glu Asp Glu Gly Thr Glu Gly Glu Asp Glu
195 200 205

ggg cct cag tgg tcg ccg cag gac ccg gca ctg caa ggc gta gga cag 672
Gly Pro Gln Trp Ser Pro Gln Asp Pro Ala Leu Gln Gly Val Gly Gln
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ccc aca gga act gga agc ata aga aag aag cga ttt gtg tcc agt cac 720
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Arg Tyr Val Glu Thr Met Leu Val Ala Asp Gln Ser Met Ala Glu Phe
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cac ggc agt ggt cta aag cat tac ctt ctc acg ttg ttt tcg gtg gca 816
His Gly Ser Gly Leu Lys His Tyr Leu Leu Thr Leu Phe Ser Val Ala
260 265 270

gcc aga ttg tac aaa cac ccc agc att cgt aat tca gtt agc ctg gtg 864
Ala Arg Leu Tyr Lys His Pro Ser Ile Arg Asn Ser Val Ser Leu Val
275 280 285

gtg gtg aag atc ttg gtc atc cac gat gaa cag aag ggg ccg gaa gtg 912
Val Val Lys Ile Leu Val Ile His Asp Glu Gln Lys Gly Pro Glu Val

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acc tcc aat gct gcc ctc act ctg cgg aac ttt tgc aac tgg cag aag   960
Thr Ser Asn Ala Ala Leu Thr Leu Arg Asn Phe Cys Asn Trp Gln Lys
305                 310                 315                 320

cag cac aac cca ccc agt gac cgg gat gca gag cac tat gac aca gca   1008
Gln His Asn Pro Pro Ser Asp Arg Asp Ala Glu His Tyr Asp Thr Ala
                325                 330                 335

att ctt ttc acc aga cag gac ttg tgt ggg tcc cag aca tgt gat act   1056
Ile Leu Phe Thr Arg Gln Asp Leu Cys Gly Ser Gln Thr Cys Asp Thr
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Ser Val Ile Glu Asp Asp Gly Leu Gln Ala Ala Phe Thr Thr Ala His
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gaa tta ggc cac gtg ttt aac atg cca cat gat gat gca aag cag tgt   1200
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gcc agc ctt aat ggt gtg aac cag gat tcc cac atg atg gcg tca atg   1248
Ala Ser Leu Asn Gly Val Asn Gln Asp Ser His Met Met Ala Ser Met
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ctt tcc aac ctg gac cac agc cag cct tgg tct cct tgc agt gcc tac   1296
Leu Ser Asn Leu Asp His Ser Gln Pro Trp Ser Pro Cys Ser Ala Tyr
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atg att aca tca ttt ctg gat aat ggt cat ggg gaa tgt ttg atg gac   1344
Met Ile Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu Met Asp
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aag cct cag aat ccc ata cag ctc cca ggc gat ctc cct ggc acc tcg   1392
Lys Pro Gln Asn Pro Ile Gln Leu Pro Gly Asp Leu Pro Gly Thr Ser
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cac tgc cct gat gca gcc agc aca tgt agc acc ttg tgg tgt acc ggc   1488
His Cys Pro Asp Ala Ala Ser Thr Cys Ser Thr Leu Trp Cys Thr Gly
                485                 490                 495

acc tct ggt ggg gtg ctg gtg tgt caa acc aaa cac ttc ccg tgg gcg   1536
Thr Ser Gly Gly Val Leu Val Cys Gln Thr Lys His Phe Pro Trp Ala
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gat ggc acc agc tgt gga gaa ggg aaa tgg tgt atc aac ggc aag tgt   1584
Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Ile Asn Gly Lys Cys
        515                 520                 525

gtg aac aaa acc gac aga aag cat ttt gat acg cct ttt cat gga agc   1632
Val Asn Lys Thr Asp Arg Lys His Phe Asp Thr Pro Phe His Gly Ser
    530                 535                 540

tgg gga atg tgg ggg cct tgg gga gac tgt tcg aga acg tgc ggt gga   1680
Trp Gly Met Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly
545                 550                 555                 560

gga gtc cag tac acg atg agg gaa tgt gac aac cca gtc cca aag aat   1728
Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro Lys Asn
                565                 570                 575

gga ggg aag tac tgt gaa ggc aaa cga gtg cgc tac aga tcc tgt aac   1776
Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser Cys Asn
            580                 585                 590

ctt gag gac tgt cca gac aat aat gga aaa acc ttt aga gag gaa caa   1824
Leu Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu Glu Gln
        595                 600                 605

tgt gaa gca cac aac gag ttt tca aaa gct tcc ttt ggg agt ggg cct   1872
Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Ser Gly Pro
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WO 2004/050700 PCT/US2003/038050

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tgc aag ctc atc tgc caa gcc aaa ggc att ggc tac ttc ttc gtt ttg   1968
Cys Lys Leu Ile Cys Gln Ala Lys Gly Ile Gly Tyr Phe Phe Val Leu
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cag ccc aag gtt gta gat ggt act cca tgt agc cca gat tcc acc tct   2016
Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser Thr Ser
            660                 665                 670

gtc tgt gtg caa gga cag tgt gta aaa gct ggt tgt gat cgc atc ata   2064
Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg Ile Ile
        675                 680                 685

gac tcc aaa aag aag ttt gat aaa tgt ggt gtt tgc ggg gga aat gga   2112
Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly Asn Gly
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tct act tgt aaa aaa ata tca gga tca gtt act agt gca aaa cct gga   2160
Ser Thr Cys Lys Lys Ile Ser Gly Ser Val Thr Ser Ala Lys Pro Gly
705                 710                 715                 720

tat cat gat atc atc aca att cca act gga gcc acc aac atc gaa gtg   2208
Tyr His Asp Ile Ile Thr Ile Pro Thr Gly Ala Thr Asn Ile Glu Val
                725                 730                 735

aaa cag cgg aac cag agg gga tcc agg aac aat ggc agc ttt ctt gcc   2256
Lys Gln Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe Leu Ala
            740                 745                 750

atc aaa gct gct gat ggc aca tat att ctt aat ggt gac tac act ttg   2304
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tcc acc tta gag caa gac att atg tac aaa ggt gtt gtc ttg agg tac   2352
Ser Thr Leu Glu Gln Asp Ile Met Tyr Lys Gly Val Val Leu Arg Tyr
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WO 2004/005350 PCT/US2003/020850

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                805                 810                 815

cct aaa att aaa tac acc tac ttc gta aag aag aag aag gaa tct ttc   2496
Pro Lys Ile Lys Tyr Thr Tyr Phe Val Lys Lys Lys Lys Glu Ser Phe
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aat gct atc ccc act ttt tca gca tgg gtc att gaa gag tgg ggc gaa   2544
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tgt tct aag tca tgt gaa ttg ggt tgg cag aga aga ctg gta gaa tgc   2592
Cys Ser Lys Ser Cys Glu Leu Gly Trp Gln Arg Arg Leu Val Glu Cys
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cga gac att aat gga cag cct gct tcc gag tgt gca aag gaa gtg aag   2640
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cca gcc agc acc aga cct tgt gca gac cat ccc tgc ccc cag tgg cag   2688
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ctg ggg gag tgg tca tca tgt tct aag acc tgt ggg aag ggt tac aaa   2736
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gag agc tgt gat cct tta aag aaa cct aaa cat ttc ata gac ttt tgc   2832
Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Phe Ile Asp Phe Cys
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aca atg gca gaa tgc agt taa gtggtttaag tggtgttagc tttgaggcaa      2883
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0204W050.000

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WO 2004/050850 PCT/US2003/038150

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Glu Arg Ala Pro Gly His Gly Thr Thr Arg Leu Arg Leu His Ala Phe
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Pro Ala Pro Leu Gln Phe His Leu Leu Arg Arg Asn Arg Gln Gly Asp
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Val Gly Gly Thr Cys Gly Val Val Asp Asp Glu Pro Arg Pro Thr Gly
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Lys Ala Glu Thr Glu Asp Glu Asp Glu Gly Thr Glu Gly Glu Asp Glu
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Gly Pro Gln Trp Ser Pro Gln Asp Pro Ala Leu Gln Gly Val Gly Gln
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Pro Thr Gly Thr Gly Ser Ile Arg Lys Lys Arg Phe Val Ser Ser His
225                 230                 235                 240

Arg Tyr Val Glu Thr Met Leu Val Ala Asp Gln Ser Met Ala Glu Phe
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His Gly Ser Gly Leu Lys His Tyr Leu Leu Thr Leu Phe Ser Val Ala
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Ala Arg Leu Tyr Lys His Pro Ser Ile Arg Asn Ser Val Ser Leu Val
        275                 280                 285

Val Val Lys Ile Leu Val Ile His Asp Glu Gln Lys Gly Pro Glu Val
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Thr Ser Asn Ala Ala Leu Thr Leu Arg Asn Phe Cys Asn Trp Gln Lys
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0203450 - 2003-05-20

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Leu Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ser Arg Ser Cys
        355                 360                 365

Ser Val Ile Glu Asp Asp Gly Leu Gln Ala Ala Phe Thr Thr Ala His
    370                 375                 380

Glu Leu Gly His Val Phe Asn Met Pro His Asp Asp Ala Lys Gln Cys
385                 390                 395                 400

Ala Ser Leu Asn Gly Val Asn Gln Asp Ser His Met Met Ala Ser Met
                405                 410                 415

Leu Ser Asn Leu Asp His Ser Gln Pro Trp Ser Pro Cys Ser Ala Tyr
            420                 425                 430

Met Ile Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu Met Asp
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Lys Pro Gln Asn Pro Ile Gln Leu Pro Gly Asp Leu Pro Gly Thr Ser
    450                 455                 460

Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu Asp Ser Lys
465                 470                 475                 480

His Cys Pro Asp Ala Ala Ser Thr Cys Ser Thr Leu Trp Cys Thr Gly
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Thr Ser Gly Gly Val Leu Val Cys Gln Thr Lys His Phe Pro Trp Ala
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Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Ile Asn Gly Lys Cys
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0204060-0204080

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Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser Cys Asn
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Leu Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu Glu Gln
        595                 600                 605

Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Ser Gly Pro
    610                 615                 620

Ala Val Glu Trp Ile Pro Lys Tyr Ala Gly Val Ser Pro Lys Asp Arg
625                 630                 635                 640

Cys Lys Leu Ile Cys Gln Ala Lys Gly Ile Gly Tyr Phe Phe Val Leu
                645                 650                 655

Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser Thr Ser
            660                 665                 670

Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg Ile Ile
        675                 680                 685

Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly Asn Gly
    690                 695                 700

Ser Thr Cys Lys Lys Ile Ser Gly Ser Val Thr Ser Ala Lys Pro Gly
705                 710                 715                 720

Tyr His Asp Ile Ile Thr Ile Pro Thr Gly Ala Thr Asn Ile Glu Val
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Lys Gln Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe Leu Ala
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20020060030

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Ile Lys Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asp Tyr Thr Leu
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Ser Thr Leu Glu Gln Asp Ile Met Tyr Lys Gly Val Val Leu Arg Tyr
    770                 775                 780

Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser Pro Leu
785                 790                 795                 800

Lys Glu Pro Leu Thr Ile Gln Val Leu Thr Val Gly Asn Ala Leu Arg
                805                 810                 815

Pro Lys Ile Lys Tyr Thr Tyr Phe Val Lys Lys Lys Lys Glu Ser Phe
            820                 825                 830

Asn Ala Ile Pro Thr Phe Ser Ala Trp Val Ile Glu Glu Trp Gly Glu
        835                 840                 845

Cys Ser Lys Ser Cys Glu Leu Gly Trp Gln Arg Arg Leu Val Glu Cys
    850                 855                 860

Arg Asp Ile Asn Gly Gln Pro Ala Ser Glu Cys Ala Lys Glu Val Lys
865                 870                 875                 880

Pro Ala Ser Thr Arg Pro Cys Ala Asp His Pro Cys Pro Gln Trp Gln
                885                 890                 895

Leu Gly Glu Trp Ser Ser Cys Ser Lys Thr Cys Gly Lys Gly Tyr Lys
            900                 905                 910

Lys Arg Ser Leu Lys Cys Leu Ser His Asp Gly Gly Val Leu Ser His
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Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Phe Ile Asp Phe Cys
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WO 94/00570 PCT/US93/05870

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  1               5                  10                  15

ctg ctg ctg ctg ctg ctg ccg ctg gcc cgc ggc gcc ccg gcc cgg ccc   96
Leu Leu Leu Leu Leu Leu Pro Leu Ala Arg Gly Ala Pro Ala Arg Pro
             20                  25                  30

gca gcc ggg ggg cag gcc tcg gag ctg gtg gtg ccc acg cgg ttg ccc   144
Ala Ala Gly Gly Gln Ala Ser Glu Leu Val Val Pro Thr Arg Leu Pro
         35                  40                  45

ggc agc gcg ggc gag ctc gcg ctc cac ctg tcc gcc ttc ggc aag ggc   192
Gly Ser Ala Gly Glu Leu Ala Leu His Leu Ser Ala Phe Gly Lys Gly
     50                  55                  60
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ttc gtg ttg cgc ctg gcg ccc gac gac agc ttc ctg gcg ccc gag ttc   240
Phe Val Leu Arg Leu Ala Pro Asp Asp Ser Phe Leu Ala Pro Glu Phe
 65                  70                  75                  80

aag atc gag cgc ctc ggg ggc tcc ggc cgg gcg acc ggg ggc gag cgg   288
Lys Ile Glu Arg Leu Gly Gly Ser Gly Arg Ala Thr Gly Gly Glu Arg
                 85                  90                  95

ggg ctg cgc ggc tgt ttt ttt tcc ggc acc gtg aat ggg gag ccc gag   336
Gly Leu Arg Gly Cys Phe Phe Ser Gly Thr Val Asn Gly Glu Pro Glu
            100                 105                 110

tcg ctg gcg gcg gtc agc ctg tgc cgc ggg ctg agc ggc tcc ttc ctg   384
Ser Leu Ala Ala Val Ser Leu Cys Arg Gly Leu Ser Gly Ser Phe Leu
        115                 120                 125

ctg gac ggc gag gag ttc acc atc cag ccg cag ggc gcg ggg ggc tcc   432
Leu Asp Gly Glu Glu Phe Thr Ile Gln Pro Gln Gly Ala Gly Gly Ser
    130                 135                 140

ctg gct cag ccg cac cgc ctg cag cgc tgg ggt ccc gcc gga gcc cgc   480
Leu Ala Gln Pro His Arg Leu Gln Arg Trp Gly Pro Ala Gly Ala Arg
145                 150                 155                 160

ccc ctc ccg cga gga ccc gag tgg gag gtg gag acg gga gag ggt cag   528
Pro Leu Pro Arg Gly Pro Glu Trp Glu Val Glu Thr Gly Glu Gly Gln
                165                 170                 175

agg cag gag aga gga gac cac cag gag gac agc gag gag gag agc caa   576
Arg Gln Glu Arg Gly Asp His Gln Glu Asp Ser Glu Glu Glu Ser Gln
            180                 185                 190

gaa gag gag gca gaa ggc gct agc gag ccg cca ccg ccc ctg ggg gcc   624
Glu Glu Glu Ala Glu Gly Ala Ser Glu Pro Pro Pro Pro Leu Gly Ala
        195                 200                 205

acg agt agg acc aag cgg ttt gtg tct gag gcg cgc ttc gtg gag acg   672
Thr Ser Arg Thr Lys Arg Phe Val Ser Glu Ala Arg Phe Val Glu Thr
    210                 215                 220
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EP 0 640 140 B1

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ctg ctg gtg gcc gat gcg tcc atg gct gcc ttc tac ggg gcc gac ctg   720
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cag aac cac atc ctg acg tta atg tct gtg gca gcc cga atc tac aag   768
Gln Asn His Ile Leu Thr Leu Met Ser Val Ala Ala Arg Ile Tyr Lys
                245                 250                 255

cac ccc agc atc aag aat tcc atc aac ctg atg gtg gta aaa gtg ctg   816
His Pro Ser Ile Lys Asn Ser Ile Asn Leu Met Val Val Lys Val Leu
            260                 265                 270

atc gta gaa gat gaa aaa tgg ggc cca gag gtg tcc gac aat ggg ggg   864
Ile Val Glu Asp Glu Lys Trp Gly Pro Glu Val Ser Asp Asn Gly Gly
        275                 280                 285

ctt aca ctg cgt aac ttc tgc aac tgg cag cgg cgt ttc aac cag ccc   912
Leu Thr Leu Arg Asn Phe Cys Asn Trp Gln Arg Arg Phe Asn Gln Pro
    290                 295                 300

agc gac cgc cac cca gag cac tac gac acg gcc atc ctg ctc acc aga   960
Ser Asp Arg His Pro Glu His Tyr Asp Thr Ala Ile Leu Leu Thr Arg
305                 310                 315                 320

cag aac ttc tgt ggg cag gag ggg ctg tgt gac acc ctg ggt gtg gca  1008
Gln Asn Phe Cys Gly Gln Glu Gly Leu Cys Asp Thr Leu Gly Val Ala
                325                 330                 335

gac atc ggg acc att tgt gac ccc aac aaa agc tgc tcc gtg atc gag  1056
Asp Ile Gly Thr Ile Cys Asp Pro Asn Lys Ser Cys Ser Val Ile Glu
            340                 345                 350

gat gag ggg ctc cag gcg gcc cac acc ctg gcc cat gaa cta ggg cac  1104
Asp Glu Gly Leu Gln Ala Ala His Thr Leu Ala His Glu Leu Gly His
        355                 360                 365

gtc ctc agc atg ccc cac gac gac tcc aag ccc tgc aca cgg ctc ttc  1152
Val Leu Ser Met Pro His Asp Asp Ser Lys Pro Cys Thr Arg Leu Phe
    370                 375                 380

ggg ccc atg ggc aag cac cac gtg atg gca ccg ctg ttc gtc cac ctg  1200
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0503405.0050

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Gly Pro Met Gly Lys His His Val Met Ala Pro Leu Phe Val His Leu
385                 390                 395                 400

aac cag acg ctg ccc tgg tcc ccc tgc agc gcc atg tat ctc aca gag   1248
Asn Gln Thr Leu Pro Trp Ser Pro Cys Ser Ala Met Tyr Leu Thr Glu
                405                 410                 415

ctt ctg gac ggc ggg cac gga gac tgt ctc ctg gat gcc cct ggt gcg   1296
Leu Leu Asp Gly Gly His Gly Asp Cys Leu Leu Asp Ala Pro Gly Ala
            420                 425                 430

gcc ctg ccc ctc ccc aca ggc ctc ccg ggc cgc atg gcc ctg tac cag   1344
Ala Leu Pro Leu Pro Thr Gly Leu Pro Gly Arg Met Ala Leu Tyr Gln
        435                 440                 445

ctg gac cag cag tgc agg cag atc ttt ggg ccg gat ttc cgc cac tgc   1392
Leu Asp Gln Gln Cys Arg Gln Ile Phe Gly Pro Asp Phe Arg His Cys
    450                 455                 460

ccc aac acc tct gct cag gac gtc tgc gcc cag ctt tgg tgc cac act   1440
Pro Asn Thr Ser Ala Gln Asp Val Cys Ala Gln Leu Trp Cys His Thr
465                 470                 475                 480

gat ggg gct gag ccc ctg tgc cac acg aag aat ggc agc ctg ccc tgg   1488
Asp Gly Ala Glu Pro Leu Cys His Thr Lys Asn Gly Ser Leu Pro Trp
                485                 490                 495

gct gac ggc acg ccg tgc ggg cct ggg cac ctc tgc tca gaa ggc agc   1536
Ala Asp Gly Thr Pro Cys Gly Pro Gly His Leu Cys Ser Glu Gly Ser
            500                 505                 510

tgt cta cct gag gag gaa gtg gag agg ccc aag ccc gtg gta gat gga   1584
Cys Leu Pro Glu Glu Glu Val Glu Arg Pro Lys Pro Val Val Asp Gly
        515                 520                 525

ggc tgg gca ccg tgg gga ccc tgg gga gaa tgt tct cgg acc tgt gga   1632
Gly Trp Ala Pro Trp Gly Pro Trp Gly Glu Cys Ser Arg Thr Cys Gly
    530                 535                 540

gga gga gta cag ttt tca cac cgt gag tgc aag gac ccc gag cct cag   1680
Gly Gly Val Gln Phe Ser His Arg Glu Cys Lys Asp Pro Glu Pro Gln
```

09604560 - 020404

```
545                 550                 555                 560

aat gga gga aga tac tgc ctg ggt cgg aga gcc aag tac cag tca tgc   1728
Asn Gly Gly Arg Tyr Cys Leu Gly Arg Arg Ala Lys Tyr Gln Ser Cys
                565                 570                 575

cac acg gag gaa tgc ccc cct gac ggg aaa agc ttc agg gag cag cag   1776
His Thr Glu Glu Cys Pro Pro Asp Gly Lys Ser Phe Arg Glu Gln Gln
            580                 585                 590

tgt gag aag tat aat gcc tac aat tac act gac atg gac ggg aat ctc   1824
Cys Glu Lys Tyr Asn Ala Tyr Asn Tyr Thr Asp Met Asp Gly Asn Leu
        595                 600                 605

ctg cag tgg gtc ccc aag tat gct ggg gtg tcc ccc cgg gac cgc tgc   1872
Leu Gln Trp Val Pro Lys Tyr Ala Gly Val Ser Pro Arg Asp Arg Cys
    610                 615                 620

aag ttg ttc tgc cga gcc cgg ggg agg agc gag ttc aaa gtg ttc gag   1920
Lys Leu Phe Cys Arg Ala Arg Gly Arg Ser Glu Phe Lys Val Phe Glu
625                 630                 635                 640

gcc aag gtg att gat ggc acc ctg tgt ggg cca gaa aca ctg gcc atc   1968
Ala Lys Val Ile Asp Gly Thr Leu Cys Gly Pro Glu Thr Leu Ala Ile
                645                 650                 655

tgt gtc cgt ggc cag tgt gtc aag gcc ggc tgt gac cat gtg gtg gac   2016
Cys Val Arg Gly Gln Cys Val Lys Ala Gly Cys Asp His Val Val Asp
            660                 665                 670

tcg cct cgg aag ctg gac aaa tgc ggg gtg tgt ggg ggc aaa ggc aac   2064
Ser Pro Arg Lys Leu Asp Lys Cys Gly Val Cys Gly Gly Lys Gly Asn
        675                 680                 685

tcc tgc agg aag gtc tcc ggg tcc ctc acc ccc acc aat tat ggc tac   2112
Ser Cys Arg Lys Val Ser Gly Ser Leu Thr Pro Thr Asn Tyr Gly Tyr
    690                 695                 700

aat gac att gtc acc atc cca gct ggt gcc act aat att gac gtg aag   2160
Asn Asp Ile Val Thr Ile Pro Ala Gly Ala Thr Asn Ile Asp Val Lys
705                 710                 715                 720
```

```
cag cgg agc cac ccg ggt gtg cag aac gat ggg aac tac ctg gcg ctg   2208
Gln Arg Ser His Pro Gly Val Gln Asn Asp Gly Asn Tyr Leu Ala Leu
                725                 730                 735

aag acg gct gat ggg cag tac ctg ctc aac ggc aac ctg gcc atc tct   2256
Lys Thr Ala Asp Gly Gln Tyr Leu Leu Asn Gly Asn Leu Ala Ile Ser
            740                 745                 750

gcc ata gag cag gac atc ttg gtg aag ggg acc atc ctg aag tac agc   2304
Ala Ile Glu Gln Asp Ile Leu Val Lys Gly Thr Ile Leu Lys Tyr Ser
        755                 760                 765

ggc tcc atc gcc acc ctg gag cgc ctg cag agc ttc cgg ccc ttg cca   2352
Gly Ser Ile Ala Thr Leu Glu Arg Leu Gln Ser Phe Arg Pro Leu Pro
    770                 775                 780

gag cct ctg aca gtg cag ctc ctg aca gtc cct ggc gag gtc ttc ccc   2400
Glu Pro Leu Thr Val Gln Leu Leu Thr Val Pro Gly Glu Val Phe Pro
785                 790                 795                 800

cca aaa gtc aaa tac acc ttc ttt gtt cct aat gac gtg gac ttt agc   2448
Pro Lys Val Lys Tyr Thr Phe Phe Val Pro Asn Asp Val Asp Phe Ser
                805                 810                 815

atg cag agc agc aaa gag aga gca acc acc aac atc atc cag ccg ctg   2496
Met Gln Ser Ser Lys Glu Arg Ala Thr Thr Asn Ile Ile Gln Pro Leu
            820                 825                 830

ctc cac gca cag tgg gtg ctg ggg gac tgg tct gag tgc tct agc acc   2544
Leu His Ala Gln Trp Val Leu Gly Asp Trp Ser Glu Cys Ser Ser Thr
        835                 840                 845

tgc ggg gcc ggc tgg cag agg cga act gta gag tgc agg gac ccc tcc   2592
Cys Gly Ala Gly Trp Gln Arg Arg Thr Val Glu Cys Arg Asp Pro Ser
    850                 855                 860

ggc cag gcc tct gcc acc tgc aac aag gct ctg aaa ccc gag gat gcc   2640
Gly Gln Ala Ser Ala Thr Cys Asn Lys Ala Leu Lys Pro Glu Asp Ala
865                 870                 875                 880
```

WO 2004/050705 PCT/US2003/038050

aag ccc tgc gaa agc cag ctg tgc ccc ctg tgattcaggg gggcaggggc 2690
Lys Pro Cys Glu Ser Gln Leu Cys Pro Leu
885 890

cagtcttgtg ctcctggaca tgcggtactg aggtgcagac aaggtctcca ctgtggtgac 2750

tgggtccctt ggccatatca aggcagcacg gcccacccag gcctcccatt gccgcaaccc 2810

ctccagtact gcacaaattc ctaaggggga agagaaaagg tatggggcgg caaaacctat 2870

catcaactgt ccawtgnaat ggaacttgct cgggttcaat taaaggcata agttaaagta 2930

aattcattat gatcaacaga cctcacntca tctgttgcan gatacaacta ntaaaaaaaa 2990

aaaaaaaaaa aaaaaaaa 3008

<210> 4
<211> 890
<212> PRT
<213> Homo sapiens

<400> 4
Met Phe Pro Ala Pro Ala Ala Pro Arg Trp Leu Pro Phe Leu Leu Leu
1 5 10 15

Leu Leu Leu Leu Leu Leu Pro Leu Ala Arg Gly Ala Pro Ala Arg Pro
20 25 30

Ala Ala Gly Gly Gln Ala Ser Glu Leu Val Val Pro Thr Arg Leu Pro
35 40 45

Gly Ser Ala Gly Glu Leu Ala Leu His Leu Ser Ala Phe Gly Lys Gly
50 55 60

Phe Val Leu Arg Leu Ala Pro Asp Asp Ser Phe Leu Ala Pro Glu Phe
65 70 75 80

Lys Ile Glu Arg Leu Gly Gly Ser Gly Arg Ala Thr Gly Gly Glu Arg
85 90 95

```
Gly Leu Arg Gly Cys Phe Phe Ser Gly Thr Val Asn Gly Glu Pro Glu
            100                 105                 110

Ser Leu Ala Ala Val Ser Leu Cys Arg Gly Leu Ser Gly Ser Phe Leu
        115                 120                 125

Leu Asp Gly Glu Glu Phe Thr Ile Gln Pro Gln Gly Ala Gly Gly Ser
    130                 135                 140

Leu Ala Gln Pro His Arg Leu Gln Arg Trp Gly Pro Ala Gly Ala Arg
145                 150                 155                 160

Pro Leu Pro Arg Gly Pro Glu Trp Glu Val Glu Thr Gly Glu Gly Gln
                165                 170                 175

Arg Gln Glu Arg Gly Asp His Gln Glu Asp Ser Glu Glu Glu Ser Gln
            180                 185                 190

Glu Glu Glu Ala Glu Gly Ala Ser Glu Pro Pro Pro Pro Leu Gly Ala
        195                 200                 205

Thr Ser Arg Thr Lys Arg Phe Val Ser Glu Ala Arg Phe Val Glu Thr
    210                 215                 220

Leu Leu Val Ala Asp Ala Ser Met Ala Ala Phe Tyr Gly Ala Asp Leu
225                 230                 235                 240

Gln Asn His Ile Leu Thr Leu Met Ser Val Ala Ala Arg Ile Tyr Lys
                245                 250                 255

His Pro Ser Ile Lys Asn Ser Ile Asn Leu Met Val Val Lys Val Leu
            260                 265                 270

Ile Val Glu Asp Glu Lys Trp Gly Pro Glu Val Ser Asp Asn Gly Gly
        275                 280                 285

Leu Thr Leu Arg Asn Phe Cys Asn Trp Gln Arg Arg Phe Asn Gln Pro
    290                 295                 300

Ser Asp Arg His Pro Glu His Tyr Asp Thr Ala Ile Leu Leu Thr Arg
305                 310                 315                 320
```

09/14/2000 10:07:00

```
Gln Asn Phe Cys Gly Gln Glu Gly Leu Cys Asp Thr Leu Gly Val Ala
                325                 330                 335

Asp Ile Gly Thr Ile Cys Asp Pro Asn Lys Ser Cys Ser Val Ile Glu
            340                 345                 350

Asp Glu Gly Leu Gln Ala Ala His Thr Leu Ala His Glu Leu Gly His
        355                 360                 365

Val Leu Ser Met Pro His Asp Asp Ser Lys Pro Cys Thr Arg Leu Phe
    370                 375                 380

Gly Pro Met Gly Lys His His Val Met Ala Pro Leu Phe Val His Leu
385                 390                 395                 400

Asn Gln Thr Leu Pro Trp Ser Pro Cys Ser Ala Met Tyr Leu Thr Glu
                405                 410                 415

Leu Leu Asp Gly Gly His Gly Asp Cys Leu Leu Asp Ala Pro Gly Ala
            420                 425                 430

Ala Leu Pro Leu Pro Thr Gly Leu Pro Gly Arg Met Ala Leu Tyr Gln
        435                 440                 445

Leu Asp Gln Gln Cys Arg Gln Ile Phe Gly Pro Asp Phe Arg His Cys
    450                 455                 460

Pro Asn Thr Ser Ala Gln Asp Val Cys Ala Gln Leu Trp Cys His Thr
465                 470                 475                 480

Asp Gly Ala Glu Pro Leu Cys His Thr Lys Asn Gly Ser Leu Pro Trp
                485                 490                 495

Ala Asp Gly Thr Pro Cys Gly Pro Gly His Leu Cys Ser Glu Gly Ser
            500                 505                 510

Cys Leu Pro Glu Glu Glu Val Glu Arg Pro Lys Pro Val Val Asp Gly
        515                 520                 525

Gly Trp Ala Pro Trp Gly Pro Trp Gly Glu Cys Ser Arg Thr Cys Gly
```

0529050 - 0604050

530 535 540

Gly Gly Val Gln Phe Ser His Arg Glu Cys Lys Asp Pro Glu Pro Gln
545 550 555 560

Asn Gly Gly Arg Tyr Cys Leu Gly Arg Arg Ala Lys Tyr Gln Ser Cys
565 570 575

His Thr Glu Glu Cys Pro Pro Asp Gly Lys Ser Phe Arg Glu Gln Gln
580 585 590

Cys Glu Lys Tyr Asn Ala Tyr Asn Tyr Thr Asp Met Asp Gly Asn Leu
595 600 605

Leu Gln Trp Val Pro Lys Tyr Ala Gly Val Ser Pro Arg Asp Arg Cys
610 615 620

Lys Leu Phe Cys Arg Ala Arg Gly Arg Ser Glu Phe Lys Val Phe Glu
625 630 635 640

Ala Lys Val Ile Asp Gly Thr Leu Cys Gly Pro Glu Thr Leu Ala Ile
645 650 655

Cys Val Arg Gly Gln Cys Val Lys Ala Gly Cys Asp His Val Val Asp
660 665 670

Ser Pro Arg Lys Leu Asp Lys Cys Gly Val Cys Gly Gly Lys Gly Asn
675 680 685

Ser Cys Arg Lys Val Ser Gly Ser Leu Thr Pro Thr Asn Tyr Gly Tyr
690 695 700

Asn Asp Ile Val Thr Ile Pro Ala Gly Ala Thr Asn Ile Asp Val Lys
705 710 715 720

Gln Arg Ser His Pro Gly Val Gln Asn Asp Gly Asn Tyr Leu Ala Leu
725 730 735

Lys Thr Ala Asp Gly Gln Tyr Leu Leu Asn Gly Asn Leu Ala Ile Ser
740 745 750

```
Ala Ile Glu Gln Asp Ile Leu Val Lys Gly Thr Ile Leu Lys Tyr Ser
        755                 760                 765

Gly Ser Ile Ala Thr Leu Glu Arg Leu Gln Ser Phe Arg Pro Leu Pro
    770                 775                 780

Glu Pro Leu Thr Val Gln Leu Leu Thr Val Pro Gly Glu Val Phe Pro
785                 790                 795                 800

Pro Lys Val Lys Tyr Thr Phe Phe Val Pro Asn Asp Val Asp Phe Ser
                805                 810                 815

Met Gln Ser Ser Lys Glu Arg Ala Thr Thr Asn Ile Ile Gln Pro Leu
            820                 825                 830

Leu His Ala Gln Trp Val Leu Gly Asp Trp Ser Glu Cys Ser Ser Thr
        835                 840                 845

Cys Gly Ala Gly Trp Gln Arg Arg Thr Val Glu Cys Arg Asp Pro Ser
    850                 855                 860

Gly Gln Ala Ser Ala Thr Cys Asn Lys Ala Leu Lys Pro Glu Asp Ala
865                 870                 875                 880

Lys Pro Cys Glu Ser Gln Leu Cys Pro Leu
                885                 890
```

<210> 5
<211> 1203
<212> PRT
<213> Bovine

<400> 5

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Met Asp Pro Pro Ala Gly Ala Ala Gly Arg Leu Leu Cys Pro Ala Leu
  1               5                  10                  15

Leu Leu Leu Leu Leu Leu Pro Leu Pro Ala Asp Ala Arg Leu Ala Ala
            20                  25                  30

Ala Ala Ala Asp Pro Pro Gly Gly Pro Gln Gly His Gly Ala Glu Arg
```

```
         35                  40                  45

Ile Leu Ala Val Pro Val Arg Thr Asp Ala Gln Gly Arg Leu Val Ser
     50                  55                  60

His Val Val Ser Ala Ala Thr Ala Pro Ala Gly Val Arg Thr Arg Arg
 65                  70                  75                  80

Ala Ala Pro Ala Gln Ile Pro Gly Leu Ser Gly Gly Ser Glu Glu Asp
                 85                  90                  95

Pro Gly Gly Arg Leu Phe Tyr Asn Val Thr Val Phe Gly Arg Asp Leu
            100                 105                 110

His Leu Arg Leu Arg Pro Asn Ala Arg Leu Val Ala Pro Gly Ala Thr
        115                 120                 125

Val Glu Trp Gln Gly Glu Ser Gly Ala Thr Arg Val Glu Pro Leu Leu
    130                 135                 140

Gly Thr Cys Leu Tyr Val Gly Asp Val Ala Gly Leu Ala Glu Ser Ser
145                 150                 155                 160

Ser Val Ala Leu Ser Asn Cys Asp Gly Leu Ala Gly Leu Ile Arg Met
                165                 170                 175

Glu Glu Glu Glu Phe Phe Ile Glu Pro Leu Glu Lys Gly Leu Ala Ala
            180                 185                 190

Lys Glu Ala Glu Gln Gly Arg Val His Val Val Tyr His Arg Pro Thr
        195                 200                 205

Thr Ser Arg Pro Pro Pro Leu Gly Gln Ala Leu Asp Thr Gly Ile Ser
    210                 215                 220

Ala Asp Ser Leu Asp Ser Leu Ser Arg Ala Leu Gly Val Leu Glu Glu
225                 230                 235                 240

Arg Val Asn Ser Ser Arg Arg Arg Met Arg Arg His Ala Ala Asp Asp
                245                 250                 255
```

SUBSTITUTE SHEET (RULE 26)

```
Asp Tyr Asn Ile Glu Val Leu Leu Gly Val Asp Asp Ser Val Val Gln
            260                 265                 270

Phe His Gly Thr Glu His Val Gln Lys Tyr Leu Leu Thr Leu Met Asn
        275                 280                 285

Ile Val Asn Glu Ile Tyr His Asp Glu Ser Leu Gly Ala His Ile Asn
    290                 295                 300

Val Val Leu Val Arg Ile Ile Leu Leu Ser Tyr Gly Lys Ser Met Ser
305                 310                 315                 320

Leu Ile Glu Ile Gly Asn Pro Ser Gln Ser Leu Glu Asn Val Cys Arg
                325                 330                 335

Trp Ala Tyr Leu Gln Gln Lys Pro Asp Thr Asp His Asp Glu Tyr His
            340                 345                 350

Asp His Ala Ile Phe Leu Thr Arg Gln Asp Phe Gly Pro Ser Gly Met
        355                 360                 365

Gln Gly Tyr Ala Pro Val Thr Gly Met Cys His Pro Val Arg Ser Cys
    370                 375                 380

Thr Leu Asn His Glu Asp Gly Phe Ser Ser Ala Phe Val Val Ala His
385                 390                 395                 400

Glu Thr Gly His Val Leu Gly Met Glu His Asp Gly Gln Gly Asn Arg
                405                 410                 415

Cys Gly Asp Glu Val Arg Leu Gly Ser Ile Met Ala Pro Leu Val Gln
            420                 425                 430

Ala Ala Phe His Arg Phe His Trp Ser Arg Cys Ser Gln Gln Glu Leu
        435                 440                 445

Ser Arg Tyr Leu His Ser Tyr Asp Cys Leu Arg Asp Asp Pro Phe Thr
    450                 455                 460

His Asp Trp Pro Ala Leu Pro Gln Leu Pro Gly Leu His Tyr Ser Met
465                 470                 475                 480
```

WO 2004/005350 PCT/US2003/020850

```
Asn Glu Gln Cys Arg Phe Asp Phe Gly Leu Gly Tyr Met Met Cys Thr
                485                 490                 495

Ala Phe Arg Thr Phe Asp Pro Cys Lys Gln Leu Trp Cys Ser His Pro
            500                 505                 510

Asp Asn Pro Tyr Phe Cys Lys Thr Lys Lys Gly Pro Pro Leu Asp Gly
        515                 520                 525

Thr Met Cys Ala Pro Gly Lys His Cys Phe Lys Gly His Cys Ile Trp
    530                 535                 540

Leu Thr Pro Asp Ile Leu Lys Arg Asp Gly Asn Trp Gly Ala Trp Ser
545                 550                 555                 560

Pro Phe Gly Ser Cys Ser Arg Thr Cys Gly Thr Gly Val Lys Phe Arg
                565                 570                 575

Thr Arg Gln Cys Asp Asn Pro His Pro Ala Asn Gly Gly Arg Thr Cys
            580                 585                 590

Ser Gly Leu Ala Tyr Asp Phe Gln Leu Cys Asn Ser Gln Asp Cys Pro
        595                 600                 605

Asp Ala Leu Ala Asp Phe Arg Glu Glu Gln Cys Arg Gln Trp Asp Leu
    610                 615                 620

Tyr Phe Glu His Gly Asp Ala Gln His His Trp Leu Pro His Glu His
625                 630                 635                 640

Arg Asp Ala Lys Glu Arg Cys His Leu Tyr Cys Glu Ser Lys Glu Thr
                645                 650                 655

Gly Glu Val Val Ser Met Lys Arg Met Val His Asp Gly Thr Arg Cys
            660                 665                 670

Ser Tyr Lys Asp Ala Phe Ser Leu Cys Val Arg Gly Asp Cys Arg Lys
        675                 680                 685

Val Gly Cys Asp Gly Val Ile Gly Ser Ser Lys Gln Glu Asp Lys Cys
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WO 94/15630 PCT/US93/12350

690 695 700

Gly Val Cys Gly Gly Asp Asn Ser His Cys Lys Val Val Lys Gly Thr
705 710 715 720

Phe Ser Arg Ser Pro Lys Lys Leu Gly Tyr Ile Lys Met Phe Glu Ile
725 730 735

Pro Ala Gly Ala Arg His Leu Leu Ile Gln Glu Ala Asp Thr Thr Ser
740 745 750

His His Leu Ala Val Lys Asn Leu Glu Thr Gly Lys Phe Ile Leu Asn
755 760 765

Glu Glu Asn Asp Val Asp Pro Asn Ser Lys Thr Phe Ile Ala Met Gly
770 775 780

Val Glu Trp Glu Tyr Arg Asp Glu Asp Gly Arg Glu Thr Leu Gln Thr
785 790 795 800

Met Gly Pro Leu His Gly Thr Ile Thr Val Leu Val Ile Pro Glu Gly
805 810 815

Asp Ala Arg Ile Ser Leu Thr Tyr Lys Tyr Met Ile His Glu Asp Ser
820 825 830

Leu Asn Val Asp Asp Asn Asn Val Leu Glu Asp Asp Ser Val Gly Tyr
835 840 845

Glu Trp Ala Leu Lys Lys Trp Ser Pro Cys Ser Lys Pro Cys Gly Gly
850 855 860

Gly Ser Gln Phe Thr Lys Tyr Gly Cys Arg Arg Arg Leu Asp His Lys
865 870 875 880

Met Val His Arg Gly Phe Cys Asp Ser Val Ser Lys Pro Lys Ala Ile
885 890 895

Arg Arg Thr Cys Asn Pro Gln Glu Cys Ser Gln Pro Val Trp Val Thr
900 905 910

```
Gly Glu Trp Glu Pro Cys Ser Arg Ser Cys Gly Arg Thr Gly Met Gln
        915                 920                 925

Val Arg Ser Val Arg Cys Val Gln Pro Leu His Asn Asn Thr Thr Arg
    930                 935                 940

Ser Val His Thr Lys His Cys Asn Asp Ala Arg Pro Glu Gly Arg Arg
945                 950                 955                 960

Ala Cys Asn Arg Glu Leu Cys Pro Gly Arg Trp Arg Ala Gly Ser Trp
                965                 970                 975

Ser Gln Cys Ser Val Thr Cys Gly Asn Gly Thr Gln Glu Arg Pro Val
            980                 985                 990

Leu Cys Arg Thr Ala Asp Asp Ser Phe Gly Val Cys Arg Glu Glu Arg
        995                1000                1005

Pro Glu Thr Ala Arg Ile Cys Arg Leu Gly Pro Cys Pro Arg Asn Thr
   1010                1015                1020

Ser Asp Pro Ser Lys Lys Ser Tyr Val Val Gln Trp Leu Ser Arg Pro
1025                1030                1035                1040

Asp Pro Asn Ser Pro Val Gln Glu Thr Ser Ser Lys Gly Arg Cys Gln
               1045                1050                1055

Gly Asp Lys Ser Val Phe Cys Arg Met Glu Val Leu Ser Arg Tyr Cys
           1060                1065                1070

Ser Ile Pro Gly Tyr Asn Lys Leu Cys Cys Lys Ser Cys Asn Pro His
       1075                1080                1085

Asp Asn Leu Thr Asp Val Asp Asp Arg Ala Glu Pro Pro Ser Gly Lys
   1090                1095                1100

His Asn Asp Ile Glu Glu Leu Met Pro Thr Leu Ser Val Pro Thr Leu
1105                1110                1115                1120

Val Met Glu Val Gln Pro Pro Pro Gly Ile Pro Leu Glu Val Pro Leu
               1125                1130                1135
```

WO 2004/050700 PCT/US2003/038450

Asn Thr Ser Ser Thr Asn Ala Thr Glu Asp His Pro Glu Thr Asn Ala
1140 1145 1150

Val Asp Val Pro Tyr Lys Ile Pro Gly Leu Glu Asp Glu Val Gln Pro
1155 1160 1165

Pro Asn Leu Ile Pro Arg Arg Pro Ser Pro Tyr Glu Lys Thr Arg Asn
1170 1175 1180

Gln Arg Ile Gln Glu Leu Ile Asp Glu Met Arg Lys Lys Glu Met Leu
1185 1190 1195 1200

Gly Lys Phe

WO 2004/005350 PCT/US2003/020855

<210> 6
<211> 50
<212> PRT
<213> Homo sapiens

<400> 6
Asp Asp Gly Trp Ser Pro Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser
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Cys Gly Asn Gly Ile Gln Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn
20 25 30

Asn Arg Cys Glu Gly Ser Ser Val Gln Thr Arg Thr Cys His Ile Gln
35 40 45

Glu Cys
50

<210> 7
<211> 57
<212> PRT
<213> Homo sapiens

<400> 7

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Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser Val Thr
  1               5                  10                  15

Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser Pro Ser
             20                  25                  30

Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu Thr Lys
         35                  40                  45

Ala Cys Lys Lys Asp Ala Cys Pro Ile
     50                  55
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WO 2004/050696 PCT/US2003/038050

<210> 8
<211> 57
<212> PRT
<213> Homo sapiens

<400> 8

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Asn Gly Gly Trp Gly Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr
  1               5                  10                  15

Cys Gly Gly Gly Val Gln Lys Arg Ser Arg Leu Cys Asn Asn Pro Thr
             20                  25                  30

Pro Gln Phe Gly Gly Lys Asp Cys Val Gly Asp Val Thr Glu Asn Gln
         35                  40                  45

Ile Cys Asn Lys Gln Asp Cys Pro Ile
     50                  55
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<210> 9
<211> 50
<212> PRT
<213> Homo sapiens

<400> 9

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Glu Glu Gly Trp Ser Pro Trp Ala Glu Trp Thr Gln Cys Ser Val Thr
  1               5                  10                  15
```

```
Cys Gly Ser Gly Thr Gln Gln Arg Gly Arg Ser Cys Asp Val Thr Ser
             20                  25                  30

Asn Thr Cys Leu Gly Pro Ser Ile Gln Thr Arg Ala Cys Ser Leu Ser
         35                  40                  45

Lys Cys
     50
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<210> 10
<211> 57
<212> PRT
<213> Homo sapiens

<400> 10

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Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser Val Thr
  1               5                  10                  15

Cys Gly Val Gly Asn Ile Thr Arg Ile Arg Leu Cys Asn Ser Pro Val
             20                  25                  30

Pro Gln Met Gly Gly Lys Asn Cys Lys Gly Ser Gly Arg Glu Thr Lys
         35                  40                  45

Ala Cys Gln Gly Ala Pro Cys Pro Ile
     50                  55
```

<210> 11
<211> 56
<212> PRT
<213> Homo sapiens

<400> 11

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Asp Gly Arg Trp Ser Pro Trp Ser Pro Trp Ser Ala Cys Thr Val Thr
  1               5                  10                  15

Cys Ala Gly Gly Ile Arg Glu Arg Thr Arg Val Cys Asn Ser Pro Glu
             20                  25                  30
```

09/24/2004 10:50:20

Pro Gln Tyr Gly Gly Lys Ala Cys Val Gly Asp Val Gln Glu Arg Gln
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Met Cys Asn Lys Arg Ser Cys Pro
50 55

<210> 12
<211> 3974
<212> DNA
<213> Homo sapiens

<400> 12
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ggtcatagct gtttcctgtg tgaaattgtt atccgctcac aattccacac aacatacgag 120

ccggaagcat aaagtgtaaa gcctggggtg cctaatgagt gagctaactc acattaattg 180

cgttgcgctc actgcccgct ttccagtcgg gaaacctgtc gtgccagctg cattaatgaa 240

tcggccaacg cgcggggaga ggcggtttgc gtattgggcg ctcttccgct tcctcgctca 300

ctgactcgct gcgctcggtc gttcggctgc ggcgagcggt atcagctcac tcaaaggcgg 360

taatacggtt atccacagaa tcaggggata acgcaggaaa gaacatgtga gcaaaaggcc 420

agcaaaaggc caggaaccgt aaaaaggccg cgttgctggc gtttttccat aggctccgcc 480

cccctgacga gcatcacaaa aatcgacgct caagtcagag gtggcgaaac ccgacaggac 540

tataaagata ccaggcgttt ccccctggaa gctccctcgt gcgctctcct gttccgaccc 600

tgccgcttac cggatacctg tccgcctttc tcccttcggg aagcgtggcg ctttctcata 660

gctcacgctg taggtatctc agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc 720

acgaaccccc cgttcagccc gaccgctgcg ccttatccgg taactatcgt cttgagtcca 780

acccggtaag acacgactta tcgccactgg cagcagccac tggtaacagg attagcagag 840

cgaggtatgt aggcggtgct acagagttct tgaagtggtg gcctaactac ggctacacta 900

gaagaacagt atttggtatc tgcgctctgc tgaagccagt taccttcgga aaaagagttg 960

gtagctcttg atccggcaaa caaaccaccg ctggtagcgg tggtttttt gtttgcaagc 1020

agcagattac gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacggggt 1080

ctgacgctca gtggaacgaa aactcacgtt aagggatttt ggtcatgaga ttatcgtcga 1140

caattcgcgc gcgaaggcga agcggcatgc atttacgttg acaccatcga atggtgcaaa 1200

acctttcgcg gtatggcatg atagcgcccg gaagagagtc aattcagggt ggtgaatgtg 1260

aaaccagtaa cgttatacga tgtcgcagag tatgccggtg tctcttatca gaccgtttcc 1320

cgcgtggtga accaggccag ccacgtttct gcgaaaacgc gggaaaaagt ggaagcggcg 1380

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<211> 112
<212> DNA
<213> Homo sapiens

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caattgtgag cggataacaa tttcacacat taaagaggag aaattacata tg 112

<210> 14
<211> 542
<212> DNA
<213> Mus musculus

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<223> May be any nucleic acid

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acaacccagt cccaaagaat ggagggaagt actgtgaagg caaacgagtg cgctacagat 180

cctgtaacct tgaggactgt ccagacaata atggaaaaac ctttagagag gaacaatgtg 240

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cagattncac ctttgtctgt gtgcaaggac agtgtgttaa aagttggttg tgatccgcnt 480

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<210> 15
<211> 320
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:Unknown

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cacagtaaga acctggatgg tcaagggctc tttgagaggg ctaaagctgc gaattctttc 180

caatgccgca gaggagccgc tgtacctcaa gacaacacct ttgtacataa tgtcttgctc 240

taaggtggac aaagtgtagt caccattaag aatatatgtg ccatcagcag ctttgatggc 300

aagaaagctg cccttgttcc 320

<210> 16
<211> 316
<212> DNA
<213> Eimeria tenella

<400> 16
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gttctaagac ctgtgggaag ggttacaaaa aaagaagctt gaagtgtctg tcccatgatg 180

gaggggtgtt atctcatgag agctgtgatc ctttaaagaa acctaaacat ttcatagact 240

tttgcacaat ggcagaatgc agttaagtgg tttaagtggt gttagctttg agggcaaggc 300

aaagtgagga agggct 316

<210> 17
<211> 383
<212> DNA
<213> Caenorhabditis elegans

<220>
<221> UNSURE
<222> (160)
<223> May be any nucleic acid

<220>
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<222> (379)
<223> May be any nucleic acid

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aatgtggtgt ttgcggggga aatggatcta cttgtaaaan aatatcagga tcagttacta 180

gtgcaaaacc tgggatatca tgatatcatc acaattccaa ctgggagcca ccaacatcga 240

agtgaaacag cggaaccaga ggggatccag ggaacaatgg gcagctttct tgccatcaaa 300

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<210> 18
<211> 404
<212> DNA
<213> Crotalus atrox

<220>

<221> UNSURE
<222> (21)
<223> May be any nucleic acid

<220>
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<222> (301)
<223> May be any nucleic acid

<220>
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tggtttacaa gctgccttca ccacagccca tgaattaggc cacgtgttta acatgccaca 180

tgatggatgc aaagcagtgt gccagcctta aatggtgtga accagggatt cccacatgat 240

ggcgtcaatg ctttccaacc tgggaccaca gccagccttg ggtcctcctt gcagtggcct 300

nacatggatt gacatcattt ctgggatgaa tggtncatgg gggaatgttt tgattggaca 360

agccttcaga atnccctnac annttcccag gggttctccc tggg 404

<210> 19
<211> 152
<212> DNA
<213> Homo sapiens

<220>
<221> UNSURE
<222> (105)
<223> May be any nucleic acid

<220>
<221> UNSURE
<222> (122)
<223> May be any nucleic acid

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<222> (135)
<223> May be any nucleic acid

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gncacggcca tcctnctcac cagacagaac tt 152

<210> 20
<211> 4180
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:Unknown

<400> 20

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tctggacttg ttccccagct ccgggggcgc ttctaggtcc tgcagcagcc agcagtgcgg 180

agccaccaac tcggtgctgg aatgaaaaaa ttcccgcgcg ccagtgcaga atctttctaa 240

gtgacccgga gcttcgggtg ctagctctgc acgaactttc ccatcaaagt gatcgtgaat 300

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<210> 21
<211> 9248
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:Unknown

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gagccaccaa ctcggtgctg gaatgaaaaa attcccgcgc gccagtgcag aatctttcta 240

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tgaaagacaa gaggcgagag tgccgggagc tcctcggggg cccggcccgg ggctctgaaa 38100

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ttggagcccg cccggggtcg gagatc 38186

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ggagaaggag gaggttcagc agtcgctcga gccggtggct tttcacgact ctgacgagtg 180

tcacgtgtgc ggcatgatca tcactgactt ccccggcccc aagggccagg cggtcgaaaa 240

gcggggagtg aagaaatttt gttccaccgc cgaaatgctt ggttggtggc tgcagccgga 300

aaaccgtctg ctcgatgcca agctctacgt ccacgacatg gggcgcagcg tttgggaaaa 360

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caaaggcgcc atgggcgcgt cgcttgcaag ctttgccgag gagcaggacg ccaaggcgct 480

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cgcacacgca ggccactgag cagcagtggt ctgaacagca cacacaagaa atcgaggtaa 660

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US 2004/0005600 A1 Jan. 8, 2004

<213> Unknown

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ccgcgct 127

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<212> DNA
<213> Unknown

<220>
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cgcgcccctc cgttctcgac ctccccgacg ctgtctgaac acgcgtcgcc ggggggacgac 240

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caaggctcgc ccatcgtggg ggagaaccgg cgcgacgcta ggagagacaa gtgatccagc 360

aggagtcgcg gctcaaggtc gccgacaaca ccggtgcgaa ggaaatcctg accatccgtg 420

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<213> Homo sapiens

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<222> (558)
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cagatggnca gtgtttctgg cccacacagg gtgccatcaa tcaccttggn ctcgaacact 360

ttggaactcg ctcctccccc gggntcggga ggaacaactt gcaggggtcc cgggggggac 420

aacccagcat tcttggggga cccactgcag gaggattccc cgtccatgtc aagtgtnatt 480

ggtgggcatt attcttctca caattgntgc tccctgaagg ttttcccgnc aaggggggat 540

tccccccng ntggaatnat tggtacttgg gtctccga 578

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<211> 305
<212> DNA
<213> Homo sapiens

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<222> (128)

<223> May be any nucleic acid

<220>
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<222> (146)
<223> May be any nucleic acid

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ctggacangt tgatgatagg gtctgncgcc ccataccctc tcctcttccc ccttaggaat 180

ttgtgcagta ctggaggggt tgcggcaatg ggaggcctgg gtgggccgtg ctgccttgat 240

atggccaagg gacccagtca ccacagtgga gacccttgtc tgcacctcag taccgcatgt 300

ccagg 305

<210> 44
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ccggctggca gaggcgaact gtagagtgca gggacccctc cggtgcaggc ctctgccacc 180

tgcaacaagg ctctggaaac ccgaggatgc caagccctgg cagaaccagc tgtgcccccc 240

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<210> 45
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<212> DNA
<213> Unknown

<220>
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<212> DNA
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cgn 123

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<211> 109
<212> DNA
<213> Unknown

<220>
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agagagcagc agagcagagc agagcanagt agagnagagc anagcnnac 109

<210> 48
<211> 293
<212> DNA
<213> Homo sapiens

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<222> (86)
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ttaatcgaag tcattgggac cattttaaaa ggggcttcct ggattatagn ctt 293

<210> 49
<211> 506
<212> DNA
<213> Homo sapiens

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<222> (283)
<223> May be any nucleic acid

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<400> 49
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gcagcagcag cagcagcagc agcagcaaca gtaacagcag cagttcgtcc ggacccaacc 120

0540450.0042US0

cttctacctc ctttgagccc atcaaggcag accccacagg tgttttggaa ctccccaaag 180

agctgtcaga aatctttgat cccacacgag agtgcatgag ctcggagctg ctggaggagt 240

tgatgtcctc agaagtgttt gcccctctgc tttcgtcttt ctncaccccc gggagaccac 300

gattatatct acaacctgga cgagagtgaa ggtgtttgtg anctcttttg atgtgnctgt 360

tntnaacntt tgactgacag ggacatgcct tttttggttg ggacccagat tttttgactt 420

gggggtttnc ttgggacttt tcaaccgacc ctanagagtt nagagcaaan aggttggttt 480

ttcggcttcc ttaacgaaag ttttgg 506

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<210> 50
<211> 419
<212> DNA
<213> Homo sapiens

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<222> (137)
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WO 2004/035607 PCT/US2003/033000

<400> 50
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tgcatgctct tgtctccctt aatggagaga gtgtgacact gcttagcact tggatggctt 120

ggggtggtgg ttatgancag cagtctgtca cagctcagcg aggtgaagcc tgtgggcgtt 180

ttgctctgtg ctgaatggct cagtggccct acaaagcgga ntcagctctt ggtggctttc 240

tgttgtggtg ggctgctgnt gctgctgctg ctgctgctgc tgctgccctt gcctctaaaa 300

gaactcactt cctcttcctc ctgctgncac ctgtcttttg gcttgtggga ttggagtcat 360

ggggcccaga tggagccttg ctccntgant tatgataggc ccctcggtct cttttntnc 419

<210> 51
<211> 495
<212> DNA
<213> Saccharomyces cerevisiae

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<222> (177)
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agtccctggg actcccacct ccgagccagc tcccaccccc agcatgactg gcctgcctct 240

gtctgctctt ccaccacctc ttgcacaaag cccagtcctc cggcccagaa catcctgggc 300

ccggagttcc ttccttgcct tnaggggntt ttcagcaagt tnagttcctt gggtccttt 360

tgggaaantt naggnagttn aaggantacc aggttnttgc catnctttcc agatccaagt 420

ttnacnaaaa attttnaaca gtntaaattg ggtttnttgn ccctttnngg nggntgtttt 480

ttttttcggg tccgg 495

<210> 52
<211> 81
<212> DNA
<213> Unknown

<220>
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<222> (65)
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<223> May be any nucleic acid

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gagananata natanatata t 81

<210> 53
<211> 305
<212> DNA
<213> Homo sapiens

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<222> (11)
<223> May be any nucleic acid

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<223> May be any nucleic acid

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tnatgcagcc ccagggtttt nttaatgctc aaatggtcgc ccaacgcagc agagagctgc 120

taagtcatca cttccgacaa cagagggtgg ctataatgat gcagcagcag cagcagcagc 180

aacagcagca gcagcagcag cagcagcagc aacagcaaca gcaacagcaa cagcagcaac 240

agcagcaaac ccaggncttc agcccacctc ctaatgtgac tgcttcccnc agcatggatg 300

ggctt 305

<210> 54
<211> 307
<212> DNA
<213> Hepatitis C virus

<220>
<221> UNSURE
<222> (212)
<223> May be any nucleic acid

<400> 54
tggggtgtga agctccggtg ctggtgcggc gggggactgc ggggccagcc tcagtttaaa 60

ccccctcagc agtctttctg tcgttgccct ccacactgcg agactctgga gggcgatctg 120

gaggtctgga agataaccga ttcctgggag atttgggggt agtctccaat ctgtccctgg 180

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ctcatcttgt gacccgaagc cggcggcctt gncaggagta ttctagaatg agtgcacata 240

aaaatacctt caaacggtag cagcagcagc agcagcagca gcagcaagca gcagcagcag 300

cagcagc 307

<210> 55
<211> 88
<212> DNA
<213> Unknown

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<222> (6)
<223> May be any nucleic acid

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<220>
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tgctgctgct gctgccgntg tgngcana 88

<210> 56
<211> 346
<212> DNA
<213> Unknown

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gagggaaaaa aaaaaccggc agccactgct gaatgttggg ttcggaggct gcatccgact 180

cggtcacaag gaaaatggat tcagtttgca tctctccctc ctttaaacag cttctccggg 240

tctcagcatg ggcttccagg gcagcgattg aggagacntt accaaggngc accacacant 300

agatgctgag acntcgtgac tccaggataa gaaacattaa cngggg 346

<210> 57
<211> 496
<212> DNA
<213> Unknown

<220>
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<222> (366)
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gtcaatgggt ggctggagat gctcatggtc tatccccgga ccaacaagca gaatcagaag 180

aagaaacgga aagtngnagc cccccacacc acaggagcct gggactgcca agttgggctg 240

ttaccagcag cagcagcagc agcagcagca gcagcagcat ccccantgct ntnggaaagt 300

tcccaccacc aagtnccaca atttgggnna aaaccaaggt tgtngnagac gngntttngg 360

gatttnggca ttgtgggttg cttgcatgga aggacattng gttgtnggtn ccttggangn 420

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<212> DNA
<213> Drosophila sp.

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ttccaattag gcaggggttt gtacgctccc tgtcctatga ggaacccaga agacactcac 180

cccccattga gaagcagctc tntccagcca ttcagaaact catggtcagg agcgcagacc 240

tccacccatt gtcagagctg cctgaaaa 268

<210> 59

<211> 471
<212> DNA
<213> Homo sapiens

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<222> (249)
<223> May be any nucleic acid

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<222> (449)
<223> May be any nucleic acid

<400> 59
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agacatgctg ctgctgctgc tgctgctgcc cctgctctgg gggacaaagg ggatggaggg 120

agacagacaa tatggggatg gttacttgct gcaagtgcag gagctggtga cggtgcagga 180

gggcctgtgt gtccatgtgc cctgctcctt ctcctacccc caggatggct ggactgactc 240

tgacccagnt catggctact ggttccgggc aggagacaga ccataccaag acgctccagt 300

ggccacaaac aacccagaca gagaagtgca ggcagagacc cagggccgat tccaactcct 360

tggggacatt tggagcaacg actgcnccct gagcatcaga gacgccagga agagggataa 420

ggggtcatat ttctttcggc tagagagang aagcatgaaa tggagttaca a 471

<210> 60
<211> 379
<212> DNA
<213> Unknown

<220>
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<222> (374)
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<400> 60
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gttcaggagg catggagctg acaaccatga ggcctcggca gccaccgcca ccaccgccgc 120

cgccaccacc gtagncagca gcagcagcag cagcagcagc aagagttaac tctgacttag 180

ggaatagaga cagccagaga gaaatgtgat caatgaagga gacatctgga gtgtgcgtgc 240

ttcttcagag gggacgggtg atgggcagat ttggaaaaag caccgcagat tgggaacctt 300

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aaaacttaaa agtnggttt 379

<210> 61
<211> 255
<212> DNA
<213> Unknown

<220>
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nactgccagg gtcagacagt ccatttgctg ctgctgctgc tgctgctgct ttctcgaact 180

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aatgttcttt cctnn 255

<210> 62
<211> 5289
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:Unknown

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ctatcccgtc gctgcgccct tgtcgccggc cccggccgct gcatccgcgt ccgcacaggc 120

tccttgctgg gcacaaatag ctccaccatg gggctggcct ggggactcgg tgtcctgctc 180

ctgttgcatg cctgcggctc caaccgcatt ccagagtctg ggggagacaa cagtgtgttt 240

gacatctttg aactcaccgg agctgcccgc aagcggtctg ggcgccgact ggtgaagggc 300

cctgaccctt ctagcccagc tttccgcatc gaggatgcca acctgatccc ccctgtgcct 360

gacaagaagt tccaagacct agtggatgct gtgcgggcgg agaaaggttt cctcctcctg 420

gcctccctga ggcaaatgaa gaagacccgg ggtaccctgc tggctgtgga gcggaaagac 480

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cactctggcc aggtcttcag cgtgatctcc aatggcaagg cgggcaccct ggacctgagc 540

ctgaccgtgc aggggaagca gcatgtggtg tcggtggaag aagcactcct ggcgactggc 600

cagtggaaga gcatcaccct gtttgtgcag gaggacaggg cccagctgta catcgactgt 660

gagaagatgg agaatgcgga gctggatgtc cccatccaga gcatcttcac cagggacctg 720

gccagcatcg ccaggctccg cattgccaaa ggaggtgtca acgacaattt ccaggggtg 780

ctgcagaatg taaggtttgt ctttggaacc acaccagaag acatcctcag gaacaaaggc 840

tgctccagct ctaccagtgt ctttgtcacc cttgacaaca acgtggtgaa tgggtccagc 900

cctgccatcc gcaccgacta cattggccac aagacaaagg acctgcaagc catctgtggc 960

atctcatgtg acgagctgtc cagcatggtc ctggagctca ggggtctacg caccatcgtg 1020

accacgctgc aggacagtat ccgcaaagtg accgaagaga acaaagagct ggccaacgag 1080

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acggtggaca gctgcactga gtgtcgctgc cagaactcag ttaccatctg caaaaaagtg 1200

tcctgtccca tcatgccctg ctccaatgcc acagttccgg atggagaatg ctgcccacgg 1260

tgctggccca gcgactctgc agacgatggc tggtccccgt ggtctgagtg gacctcttgc 1320

tctgtgacct gtggcaatgg aatccagcag cgtggccgct cctgcgacag cctcaacaac 1380

agatgcgagg gctcctctgt gcagacgcgg acctgccaca tccaggagtg tgacaagaga 1440

tttaaacagg atggcggctg gagccactgg tccccatggt catcttgctc cgtaacatgt 1500

ggagacggtg tgatcacaag gatccggctc tgcaactccc ccagccccca gatgaatggg 1560

aagccatgtg agggcaaagc ccgggagacc aaagcctgcc agaaagactc ctgccccatc 1620

aatggaggct ggggaccttg gtcaccatgg gacatctgtt ctgtcacctg tggaggaggg 1680

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gtacagaaac gtagccggct ctgcaacaac cccaaacccc agtttggagg caaggactgc 1740

gttggtgatg tgacagaaaa ccagatctgc aacaagcagg actgtcccat tgacggatgc 1800

ctgtccaatc cctgctttgc tggtgtccag tgtaccagct accctgatgg cagctggaag 1860

tgtggtgcct gtcccccagg ctatagtgga gatggagtcg agtgcaaaga cgttgatgag 1920

tgcaaagaag tccctgatgc ctgcttcaac cacaatggag agcacaggtg tgagaacaca 1980

gaccccggct acaactgcct gccctgccca ccgcgcttca ctggctcgca gcccttggc 2040

cggggcgtgg aacatgccac cgccaacaag caggtatgca agccccgaaa cccctgcaca 2100

gacgggacac acgactgcaa caagaacgcc aagtgcaact acctgggcca ctacagcgac 2160

cccatgtacc gctgcgagtg caagcctggc tacgccggca acggcatcat ctgcggggag 2220

gacacagacc tggacggctg gcccaatgag gacctgctgt gcgtggccaa cgcaacttac 2280

cactgcagaa aggataattg ccccaacctt cccaactcag ggcaggaaga ctatgacaag 2340

gatggaatcg gcgatgcctg cgatgatgac gatgacaatg ataagattcc agatgacagg 2400

gacaactgtc cattccatta caacccagcc cagtacgact atgacagaga tgacgtggga 2460

gaccgctgtg acaactgccc ctacaaccac aacccagacc aggctgacac agataacaat 2520

ggggaaggag acgcctgtgc agctgacatt gatggggaca gtatcctcaa tgaacgggac 2580

aactgccagt atgtctacaa tgtggaccag aaagacactg acatggacgg ggttggtgat 2640

cagtgtgaca actgcccccc ggaacacaat ccagaccagc tcgactctga ctcggaccgc 2700

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<212> DNA
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<213> Unknown

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<211> 745
<212> DNA
<213> Unknown

<220>

<223> Description of Unknown Organism:Unknown

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<210> 71
<211> 1986
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:Unknown

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<211> 2003
<212> DNA
<213> Unknown

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<223> May be any nucleic acid

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<222> (32)
<223> May be any nucleic acid

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agaagcccgc acgcacctcg caccatgaga tggcgacgcg ccccgcgccg ctccgggcgt 300

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aataaaagga aaaaaaaaaa aaa 2003

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<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:Unknown

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<222> (809)
<223> May be any nucleic acid

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<223> May be any nucleic acid

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<222> (811)
<223> May be any nucleic acid

SUBSTITUTE SHEET (RULE 26)

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<211> 957
<212> DNA
<213> Unknown

<220>
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<223> May be any nucleic acid

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<223> May be any nucleic acid

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<211> 1089
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:Unknown

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<222> (850)
<223> May be any nucleic acid

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<210> 76
<211> 1985
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:Unknown

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gattactttg agtattttgg accagacttc aaactgcata ttagtccttc aaacatgaca 1260

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agaaatgtgg ctgatcataa gaaaggagca aagaaagcta gaattgaaga agataagaaa 1560

gaaacagagg acaaaaaaac agacgttaag gaagaagata aatccaagga caacagtggt 1620

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09549508.030402

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actttttcgt ttttgttttt ctgggcaagt tttattgtga gattttctaa ttatgaagca 1860

aaatttcttt tctccaccat gctttatgtg atagtattta aaattgatgt gagttattat 1920

gtcaaaaaaa ctgatctatt aaagaagtaa ttggcctttc tgagctgaaa aaaaaaaaaa 1980

aaaag 1985

<210> 77
<211> 476
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:Unknown

<400> 77
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cctgtagatc cgagcaccag ccggcgcttc agcccccccc ccagcagcct gcagcccggc 120

aaaatgagcg acgtgagccc ggtggtggct gcgcaacagc agcagcaaca gcagcagcag 180

caacagcagc agcagcagca gcaacagcag cagcagcagc aggaggcggc ggcggcggct 240

gcggcggcag cggcggctgc ggcggcggca gctgcagtgc cccggttgcg gccgccccac 300

gacaaccgca ccatggtgga gatcatcgcc gaccacccgg ccgaactcgt ccgcaccgac 360

agccccaact tcctgtgctc ggtgctgccc tcgcactggc gctgcaacaa gaccctgccc 420

gtggccttca aggtaagagg ctaccccgcc ccccgccccc ggccgggagc ggcgga 476

<210> 78
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DNA Primer

<400> 78
gcattttgga tccgcctttt catg 24

<210> 79
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DNA Primer

<400> 79
gttgtgtgct gcagattgtt cc 22

<210> 80
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DNA Primer

<400> 80
gaaaaatggg gatccgaggt g 21

<210> 81
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DNA Primer

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<400> 81
gcaggagaat tccgtccatg 20

<210> 82
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (3)
<223> Can be any amino acid

<400> 82
Trp Ser Xaa Trp Ser
1 5

<210> 83
<211> 6
<212> PRT
<213> Homo sapiens

<400> 83
Cys Ser Val Thr Cys Gly
1 5

<210> 84
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (4)
<223> Can be any amino acid

<400> 84
Gly Cys Gln Xaa Arg

1 5

<210> 85
<211> 733
<212> DNA
<213> Homo sapiens

<400> 85
gggatccgga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg 60

aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga 120

tctcccggac tcctgaggtc acatgcgtgg tggtggacgt aagccacgaa gaccctgagg 180

tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240

aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300

ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca acccccatcg 360

agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420

catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct 480

atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540

ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg 600

acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc 660

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gactctagag gat 733

<210> 86
<211> 86
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DNA Primer

<400> 86
gcgcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aaatgatttc 60

cccgaaatat ctgccatctc aattag 86

<210> 87
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DNA Primer

<400> 87
gcggcaagct ttttgcaaag cctaggc 27

<210> 88
<211> 271
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR Fragment

<400> 88
ctcgagattt ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg 60

aaatatctgc catctcaatt agtcagcaac catagtcccg cccctaactc cgcccatccc 120

gcccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat 180

ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt 240

ttttggaggc ctaggctttt gcaaaaagct t 271

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<210> 89
<211> 32
<212> DNA
<213> Homo sapiens

<400> 89
gcgctcgagg gatgacagcg atagaacccc gg 32

<210> 90
<211> 31
<212> DNA
<213> Homo sapiens

<400> 90
gcgaagcttc gcgactcccc ggatccgcct c 31

<210> 91
<211> 12
<212> DNA
<213> Homo sapiens

<400> 91
ggggactttc cc 12

<210> 92
<211> 73
<212> DNA
<213> Homo sapiens

<400> 92
gcggcctcga ggggactttc ccggggactt tccggggact ttccgggact ttccatcctg 60

ccatctcaat tag 73

<210> 93
<211> 27
<212> DNA

0503505.00004/30

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR Fragment

<400> 93
gcggcaagct ttttgcaaag cctaggc 27

<210> 94
<211> 652
<212> DNA
<213> Homo sapiens

<400> 94
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ccctgcaggt ggcagcctga gaacatggcg ctgcaggggg accagggcag cgtctggttc 120
aggtggacga acagcggtgc catcacgtgg tgcttgccca tgggcccgaa gagccgtgtg 180
cagggcttgg agtcgtcgtg gggcatgctg aggacgtgcc ctagttcatg ggccagggtg 240
tgggccgcct ggagcccctc atcctcgatc acggagcagc ttttgttggg gtcacaaatg 300
gtcccgatgt ctgccacacc cagggtgtca cacagcccct cctgcccaca gaagttctgt 360
ctggtgagca ggatggccgt gtcgtagtgc tctgggtggc ggtcgctggg ctggttgaaa 420
cgccgctgcc agttgcagaa gttacgcagt gtaagccccc cattgtcgga cacctctggg 480
ccccattttt catcttctac gatcagcact tttaccacca tcangttgat ggaattcttg 540
atgctggggt gcttgtagaa tcgggcttgc cacgaaaatt aacctcagga tgtggttctg 600
caggtcggcc cgtaaagggc gccatggacg catcggccac caacagcgtt tc 652

<210> 95
<211> 716
<212> CDNA
<213> Homo sapiens

<400> 95
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gcacttttac cttttaacct atgccctcta cttgaacccg agcaaggtcc agtccactgg 120
acagttgatg atagggtctg ccgccccata ccctctcctc ttccccctta ggaatttgtg 180
cagtactgga ggggttgcgg caatgggagg cctgggtggg ccgtgctgcc ttgatatggc 240
caagggaccc agtcaccaca gtggagaccc ttgtctgcac ctcagtaccg catgtccagg 300
agcacaagac tggcccctgc ccccctgaat cacaggggac acagctggct ttcgcagggc 360
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ctgcactcta cagttcgcct ctgccagccg gccccgcagg tgctagagca ctcagaccag 480
tcccccagca cccactgtgc gtggagcagc ggctggatga tgttggtggt tgctctctct 540

ttgctgctct gcatgctaaa agtcacgtca ttaggaanca aagaaggtgt atttgacttt 600
ttgggggaa gaacctcgcc caggactgtc aggagctgca ctgtcagaag gctctgcnaa 660
ggcccngaag ctctgcangc gctccagggt ggcgatggag ccgtgtactt caggat 716

<210> 96
<211> 543
<212> DNA
<213> Homo sapiens

<400> 96
ggcataagat cacactttag ttcagagaca catttgcata aatacttgaa atggatccac 60
ccctgcaggt ggcagcctga gaacatggcg ctgcaggggg accagggcag cgtctggttc 120
aggtggacga acagcggtgc catcacgtgg tgcttgccca tggcctcgaa gagccgtgtg 180
cagggcttgg agtcgtcgtg gggcatgctg aggacgtgcc ctagttcatg ggccagggtg 240
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cccgatgtct gccacaccca gggtgtcaca cagcccctcc tgcccacaga agttctgtct 360
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ccgctgccag ttgcagaagt tacgcagtgt aaggccccca ttgtcggaca gctctggggc 480
ccatttttca tcttctacga tcagcacttt taaccacatc aggttgatgg aattcttgat 540
gcc 543

<210> 97
<211> 377
<212> DNA
<213> Mus musculus

<400> 97
gcaaagtgcc accacccttc ggatccaaaa ctagaagcaa gaggtttgtg tccgaggctc 60
gcttcgtgga aacacttctg gtggctgatg cgtccatggc tgccttctat gggaccgacc 120
tgcagaacca catcctcacg gtgatgtcaa tggcagcccg aatctacaag cacccgagca 180
tcaagaactc cgtcaacctt gtggtggtga aagtgctaat agtggaagag gaaggatggg 240
gcccggaggt gtcggacaac ggggggctca cactgcgcaa cttctgcagc tggcaacggc 300
gtttcaacaa gcccagtgac cgccacccgg agcactatga cactgccatc ttgttcacca 360
gacagaactt ctgtggg 377

<210> 98
<211> 432
<212> DNA
<213> Rattus norvegicus

<400> 98

09543505.030502

ctaaagtaca gtggttccat ggccaccctg gagcggctgc anagcttcca agccctccct 60
gagcctctta cagtacagct cctgactgtg tctggtgagg tcttccctcc aaaagtcaaa 120
tataccttct tcgtccccaa tgacacggac ttcaacgtgc agagtagcaa agaaagagca 180
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ggtcaggcct ctgacacctg tgatgaggct ctgaaacctg aggatgccaa gccctgtgga 360
agccagccat gtctcctctg atcccccttgg tggacatgtc taaggcttat ggatttgggc 420
tactggcgtt tt 432

<210> 99
<211> 354
<212> DNA
<213> Mus musculus

<400> 99
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ttcgtggaaa cacttctggt ggctgatgcg tccatggctg ccttctatgg gaccgacctg 120
cagaaccaca tcctcacggt gatgtcaatg gcagccacga atctacaagc acccgagcat 180
caggaactcc gtcaaccttg tggtggtgaa agtgctaata gtggaagagg aaggatgggg 240
cccggagtgt cggacaacgg ggggctcaca ctgcgcaact tctgcagctg gcaacggcgt 300
ttcaacaagc ccagtgaccg ccacccggag cactatgaca ctgccatctt gttc 354

<210> 100
<211> 389
<212> DNA
<213> Homo sapiens

<400> 100
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aaaagtgctg taaattcggg atttctccac cggatgctcc tgcttccgca tgggtgtcac 120
ctccatgccg ttcctncctc tttctaggga aaagcttcag ggagcagcag tgtgagaagt 180
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ctggggtgtc cccccgggac cgcctggcaa gttgttctgc cgagcccggg ggaggagcga 300
gttcaaagtg ttcgaggcca aggtgagaat caccctgggg gacttcagat ccagagatgg 360
ggggagggaa ggtcggcctg ttccccaca 389

<210> 101
<211> 305
<212> DNA
<213> Homo sapiens

<400> 101
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aagtgcactt ttacctttta acctatgccc tctacttgaa cccgagcaag gtccagtcca 120
ctggacangt tgatgatagg gtctgncgcc ccataccctc tcctcttccc ccttaggaat 180
ttgtgcagta ctggaggggt tgcggcaatg ggaggcctgg gtgggccgtg ctgccttgat 240
atggccaagg gacccagtca ccacagtgga gacccttgtc tgcacctcag taccgcatgt 300
ccagg 305

<210> 102
<211> 152
<212> DNA
<213> Homo sapiens

<400> 102
atcgtagaag atgaaaaatg gggcccagag gtgtccgaca atgggggggct tacactgcgt 60
aacttctgca actggcagcg gcgtttcaac cagcccagcg accgncaccc agagcactac 120
gncacggcca tcctnctcac cagacagaac tt 152

<210> 103
<211> 632
<212> DNA
<213> Homo sapiens

<400> 103
tttaataata ataatgcccg gggctttatt atgctgtatc actgctcaga ggttaataat 60
cctcactaac tatcctatca aatttgcaac tggcagttta ctctgatgat tcaactcctt 120
ttctatctac ccccataatc ccaccttact gatacacctc actggttact ggcaagatac 180
gctggatccc tccagccttc ttgctttccc tgcaccagcc cttcctcact ttgccttgcc 240
ctcaaagcta acaccactta aaccacttaa ctgcattctg ccattgtgca aaagtctatg 300
aaatgtttag gtttctttaa aggatcacag ctctcatgag ataacacccc tccatcatgg 360
gacagacact tcaagcttct ttttttgtaa cccttcccac aagtcttaga acatgatgac 420
cactccccca gctgccactg ggggcaggga tggtctgcac aaggtctggt gctggctggc 480
ttcacttcct ttgcacactc ggaagcaggc tgtccattaa tgtctcggca ttctaccagt 540
cttctctgcc aacccaattc acatgactta gaacattcgc cccactcttc aatgacccat 600
gctgaaaaag tggggatagc attgaaagaa tc 632

<210> 104
<211> 519
<212> DNA
<213> Homo sapiens

<400> 104
tttttttcta aacttgtaat agatgtaaca aaagaaataa taataataat gcccggggct 60
ttattatgct atatcactgc tcagaggtta ataatcctca ctaactatcc tatcaaattt 120
gcaactggca gtttactctg atgattcaac tccttttcta tctaccccca taatcccacc 180
ttactgatac acctcactgg ttactggcaa gatacgctgg atccctccag ccttcttgct 240
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tgtaaccctt cccacaggtc ttagaacatg atgaccactc ccccagctgc cactgggggc 480
agggatgtct gcacaagggc tggtgctggc tgcccggac 519

<210> 105
<211> 475
<212> DNA
<213> Homo sapiens

<400> 105
gagtcatgat gcgatcacaa ccagctttta cacactgtcc ttgcacacag acagaggtgg 60
aatctgggct acatggagta ccatctacaa ccttgggctg caaaacgaag aagtagccaa 120
tgcctttggc ttggcagatg agcttgcacc tgtcctttgg tgagacgcca gcgtacttgg 180
gaatccattc caccgcaggc ccactcccaa aggaagcttt tgaaaactcg ttgtgtgctt 240
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cacattccct catcgtgtac tggactcctc caccgcacgt tctcgaacag tctccccaag 420
gcccccacat tccccagctt ccatgaaaag gcgtatcaaa atgctttctg tcggt 475

<210> 106
<211> 455
<212> DNA
<213> Homo sapiens

<400> 106
aataataata atgcccgggg ctttattatg ctgtatcact gctcagaggt taataatcct 60
cactaactat cctatcaaat ttgcaactgg cagtttactc tgatgattca actccttttc 120
tatctacccc cataatccca ccttactgat acacctcact ggttactggc aagatacgct 180
ggatccctcc agccttcttg ctttccctgc accagccctt cctcactttg ccttgccctc 240
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tcccccagct gccactgggg gcagggatgg tctgg 455

<210> 107
<211> 515
<212> DNA
<213> Homo sapiens

<400> 107
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ggatggtctg cacaaggtct ggtgctggct ggcttcactt cctttgcaca ctcggaagca 120
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aaggtggaca aagtgtagtc accataaaga atatatgtgc catcagcagc ttttgatggc 480
aggaagctgt cattgttctt ggatccctct gttcc 515

<210> 108
<211> 359
<212> DNA
<213> Homo sapiens

<400> 108
acttcgtaaa gaagaagaag gaatctttca atgctatccc cacttttca gcatgggtca 60
ttgaagagtg gggcgaatgt tctaagtcat gtgaattggg ttggcagaga agactggtag 120
aatgccgaga cattaatgga cagcctgctt ccgagtgtgc aaaggaagtg aagccagcca 180
gcaccagacc ttgtgcagac catccctgcc cccagtggca gctgggggaa gtggtcatca 240
tgttctaaga cctgcgggaa gggttacaaa aaaagaagct ttgaagtgtc ttgtcccatg 300
atggaggggt gttatctcat tgagagctgt gatcctttaa agaaacctaa acatttcat 359

<210> 109
<211> 320
<212> DNA
<213> Homo sapiens

<400> 109
cagagaacat tcgccccact cttcaatgac ccatgctgaa aaagtgggga tagcattgaa 60
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cacagtaaga acctggatgg tcaagggctc tttgagaggg ctaaagctgc gaattctttc 180
caatgccgca gaggagccgc tgtacctcaa gacaacacct ttgtacataa tgtcttgctc 240
taaggtggac aaagtgtagt caccattaag aatatatgtg ccatcagcag ctttgatggc 300
aagaaagctg cccttgttcc 320

<210> 110
<211> 316
<212> DNA
<213> Homo sapiens

<400> 110
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gcaccagacc ttgtgcagac catccctgcc cccagtggca gctgggggag tggtcatcat 120
gttctaagac ctgtgggaag ggttacaaaa aaagaagctt gaagtgtctg tcccatgatg 180
gaggggtgtt atctcatgag agctgtgatc ctttaaagaa acctaaacat ttcatagact 240
tttgcacaat ggcagaatgc agttaagtgg tttaagtggt gttagctttg agggcaaggc 300
aaagtgagga agggct 316

<210> 111
<211> 318
<212> DNA
<213> Homo sapiens

<400> 111
agantnccga gacattaatg gacagcctgc ttccgagtgt gcaaaggaag tgaagccagc 60
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tggaggggtg ttatctcatg agagctgtga tcctttaaag aaacctaaac atttcataga 240
cttttgcaca atggcagaat ncagttaagt ggtttaagtg gtgttagctt tgagggcaag 300
gcaaagtgag gaagggct 318

<210> 112
<211> 314
<212> DNA
<213> Homo sapiens

<400> 112
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tttattatgc tatatcactg ctcagaggtt aataatcctc actaactatc ctatcaaatt 120
tgcaactggc agtttactct gatgattcaa ctccttttct atctaccccc ataatcccac 180
cttactgata cacctcactg gttactggca agatacgctg gatccctcca gccttcttgc 240
tttccctgca ccagcccttc ctcactttgc cttgccctca aagctaacac cacttaaacc 300
acttaactgc attc 314

<210> 113

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<211> 316
<212> DNA
<213> Homo sapiens

<400> 113
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tgttctaagt catgtgaatt gggttggcag aaaagacttg tagaatgccg agacattaat 120
ggacagcctg cgtccgagtg tgcaaaggaa gtgaagccag ccagcaccag accttgtgca 180
gaccatccct gcccccagtg gcagctgggg ggagtggtca tcatgttcta agacctgtgg 240
gaaggggtac aaaaaaagag gcgtgaagtg tctgtcccat gatggagggg tttatctcat 300
gagaactgtg atcctt 316

<210> 114
<211> 265
<212> DNA
<213> Homo sapiens

<400> 114
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tccccacttt ttcagcatgg gtcattgaag agtggggcga atgttctaag tcatgtgaat 180
tgggttggca gagaagactg gtagaatgcc gagacattaa tggacagcct ncttccgagt 240
gtgcaaagna agtgaagcca gccag 265

<210> 115
<211> 334
<212> DNA
<213> Mus musculus

<400> 115
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tcggaatcaa agggggtcca gaaacaatgg cagctttctg gctattagag ccgctgatgg 180
tacctatatt ctgaatggaa acttcactct gtccacacta gagcaagacc tcacctacaa 240
aggtactgtc ttaaggtaca gtggttcctc ggctgcgctg gagagaatcc gcagctttag 300
tccactcaaa gaacccttaa ccatccaggt tctt 334

<210> 116
<211> 528
<212> DNA
<213> Mus musculus

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atgaccatca tccaggaatt ctgtgatggt ggctgacgtg catttggacc agggcttgga 120
tgcatcgatg ctggtaagga ttgaagacat taaacgcttg tcttctgtag taccgaagtt 180
ctcttcacag aatttggaat cgtcatgaga aaggccaagt agatgcccaa tttcatgagc 240
cacagtgaag gctgcatgga ggccatcatc ttcaatcact gcacagctgc gctccggaga 300
acatatggtc ccaacgtctg ccattcccag ggtgtcacat gaatgatgcc cacataaatc 360
ctctcgggtg aacaggatgg ctgcatcgta gtgctcttcg tgatcatccc ctagctggtt 420
atgttggtgc tgccatttgc aaaagttctt gagggtcgtg gccgcattct tgctcacctc 480
cagactcgtg tccttgtccg tcagcaccac caccttcacc accgccag 528

<210> 117
<211> 438
<212> DNA
<213> Homo sapiens

<400> 117
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agcaattgtc aaaaaaagtt agaactatta caacccctgt ttcctggtac ttatcaaata 180
cttagtatca tgggggttgg gaaatgaaaa gtaggagaaa agtgagattt tactaagacc 240
tgttttactt tacctcacta acaatggggg gagaaaggag tacaaatagg atctttgacc 300
agcactgttt atgggctgct atgggtttca gaggaatgtt tatacattat ttctacccga 360
ggatttaaaa cttcagattg ttccaaccng gaggggaagg gcttccggcc aacgtggaat 420
taaccggcaa tnggcctt 438

<210> 118
<211> 455
<212> DNA
<213> Homo sapiens

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cttagtatca tgggggttgg gaaatgaaaa gtaggagaaa agtgagattt tactaagacc 240
tgttttactt tacctcacta acaatggggg gagaaaggag tacaaatagg atctttgacc 300
agcactgttt atggctgcta tggtttcaga gaatgtttat acattatttc taccgaggat 360
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<211> 380
<212> DNA
<213> Homo sapiens

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aagcaattgt caaaaaaagt tagaactatt acaaccccctg tttcctggta cttatcaaat 180
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cagcactgtt tatggctgct atggtttcag aggaatgttt atacattatt tctaccgaga 360
nttaaaactt cagattgttc 380

<210> 120
<211> 199
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<213> Mus musculus

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ccaggttctt atggtagga 199

<210> 121
<211> 439
<212> DNA
<213> Homo sapiens

<400> 121
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tattacaacc cctgtttcct ggtacttatc aaatacttag tatcatgggg gttgggaaat 180
gaaaagtagg aggaaagnng agnttttact aagacctgtt ttacctttac ctcactaaca 240
atgggggggag aaaggagtac aaataggatc tttgaccagc actgtttatg gctgctatgg 300
tttcagagaa tgtttataca ttatttctac cgagaattaa aacttcagat tgttcaacat 360
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gggaccatct caggtcctt 439

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<211> 471
<212> DNA
<213> Homo sapiens

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tctattacaa gtttagaaaa aacaaagcaa ttgtcaaaaa aagttagaac tattacaacc 180
cctgtttcct ggtacttatc aaatacttag tatcatgggg gttgggaaat gaaaagtagg 240
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tttatacatt atttctaccc gagaattaaa acttcagatt ggttcaacat gagagaaagg 420
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<210> 123
<211> 424
<212> DNA
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gttagaacta ttacaacccc tgtttcctgg tacttatcaa atacttagta tcatgggggt 180
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<210> 124
<211> 458
<212> DNA
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<210> 125
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<212> PRT
<213> Homo sapiens

<400> 125

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Pro Val Pro Thr Leu Leu Leu Leu Ala Ala Ala Leu Leu Ala Val Ser
         35                  40                  45

Asp Ala Leu Gly Arg Pro Ser Glu Glu Asp Glu Glu Leu Val Val Pro
     50                  55                  60

Glu Leu Glu Arg Ala Pro Gly His Gly Thr Thr Arg Leu Arg Leu His
 65                  70                  75                  80

Ala Phe Asp Gln Gln Leu Asp Leu Glu Leu Arg Pro Asp Ser Ser Phe
                 85                  90                  95

Leu Ala Pro Gly Phe Thr Leu Gln Asn Val Gly Arg Lys Ser Gly Ser
            100                 105                 110

Glu Thr Pro Leu Pro Glu Thr Asp Leu Ala His Cys Phe Tyr Ser Gly
        115                 120                 125

Thr Val Asn Gly Asp Pro Ser Ser Ala Ala Ala Leu Ser Leu Cys Glu
    130                 135                 140

Gly Val Arg Gly Ala Phe Tyr Leu Leu Gly Glu Ala Tyr Phe Ile Gln
145                 150                 155                 160

Pro Leu Pro Ala Ala Ser Glu Arg Leu Ala Thr Ala Ala Pro Gly Glu
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Lys Pro Pro Ala Pro Leu Gln Phe His Leu Leu Arg Arg Asn Arg Gln
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Gly Asp Val Gly Gly Thr Cys Gly Val Val Asp Asp Glu Pro Arg Pro
        195                 200                 205

Thr Gly Lys Ala Glu Thr Glu Asp Glu Asp Glu Gly Thr Glu Gly Glu
    210                 215                 220

Asp Glu Gly Pro Gln Trp Ser Pro Gln Asp Pro Ala Leu Gln Gly Val
225                 230                 235                 240

Gly Gln Pro Thr Gly Thr Gly Ser Ile Arg Lys Lys Arg Phe Val Ser
                245                 250                 255

Ser His Arg Tyr Val Glu Thr Met Leu Val Ala Asp Gln Ser Met Ala
            260                 265                 270

Glu Phe His Gly Ser Gly Leu Lys His Tyr Leu Leu Thr Leu Phe Ser
        275                 280                 285

Val Ala Ala Arg Leu Tyr Lys His Pro Ser Ile Arg Asn Ser Val Ser
    290                 295                 300

Leu Val Val Val Lys Ile Leu Val Ile His Asp Glu Gln Lys Gly Pro
305                 310                 315                 320

Glu Val Thr Ser Asn Ala Ala Leu Thr Leu Arg Asn Phe Cys Asn Trp
                325                 330                 335

Gln Lys Gln His Asn Pro Pro Ser Asp Arg Asp Ala Glu His Tyr Asp
            340                 345                 350

Thr Ala Ile Leu Phe Thr Arg Gln Asp Leu Cys Gly Ser Gln Thr Cys
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Asp Thr Leu Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ser Arg
    370                 375                 380
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Ser Cys Ser Val Ile Glu Asp Asp Gly Leu Gln Ala Ala Phe Thr Thr
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Ala His Glu Leu Gly His Val Phe Asn Met Pro His Asp Asp Ala Lys
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Gln Cys Ala Ser Leu Asn Gly Val Asn Gln Asp Ser His Met Met Ala
            420                 425                 430

Ser Met Leu Ser Asn Leu Asp His Ser Gln Pro Trp Ser Pro Cys Ser
        435                 440                 445

Ala Tyr Met Ile Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu
    450                 455                 460

Met Asp Lys Pro Gln Asn Pro Ile Gln Leu Pro Gly Asp Leu Pro Gly
465                 470                 475                 480

Thr Ser Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu Asp
                485                 490                 495

Ser Lys His Cys Pro Asp Ala Ala Ser Thr Cys Ser Thr Leu Trp Cys
            500                 505                 510

Thr Gly Thr Ser Gly Gly Val Leu Val Cys Gln Thr Lys His Phe Pro
        515                 520                 525

Trp Ala Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Ile Asn Gly
    530                 535                 540

Lys Cys Val Asn Lys Thr Asp Arg Lys His Phe Asp Thr Pro Phe His
545                 550                 555                 560

Gly Ser Trp Gly Met Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys
                565                 570                 575

Gly Gly Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro
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Lys Asn Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser
        595                 600                 605
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Cys Asn Leu Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu
610 615 620

Glu Gln Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Ser
625 630 635 640

Gly Pro Ala Val Glu Trp Ile Pro Lys Tyr Ala Gly Val Ser Pro Lys
645 650 655

Asp Arg Cys Lys Leu Ile Cys Gln Ala Lys Gly Ile Gly Tyr Phe Phe
660 665 670

Val Leu Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser
675 680 685

Thr Ser Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg
690 695 700

Ile Ile Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly
705 710 715 720

Asn Gly Ser Thr Cys Lys Lys Ile Ser Gly Ser Val Thr Ser Ala Lys
725 730 735

Pro Gly Tyr His Asp Ile Ile Thr Ile Pro Thr Gly Ala Thr Asn Ile
740 745 750

Glu Val Lys Gln Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe
755 760 765

Leu Ala Ile Lys Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asp Tyr
770 775 780

Thr Leu Ser Thr Leu Glu Gln Asp Ile Met Tyr Lys Gly Val Val Leu
785 790 795 800

Arg Tyr Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser
805 810 815

Pro Leu Lys Glu Pro Leu Thr Ile Gln Val Leu Thr Val Gly Asn Ala

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20 825 830

ero Lys Ile Lys Tyr Thr Tyr Phe Val Lys Lys Lys Lys Glu
835 840 845

er Phe Asn Ala Ile Pro Thr Phe Ser Ala Trp Val Ile Glu Glu Trp
850 855 860

Gly Glu Cys Ser Lys Ser Cys Glu Leu Gly Trp Gln Arg Arg Leu Val
865 870 875 880

Glu Cys Arg Asp Ile Asn Gly Gln Pro Ala Ser Glu Cys Ala Lys Glu
885 890 895

Val Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp His Pro Cys Pro Gln
900 905 910

Trp Gln Leu Gly Glu Trp Ser Ser Cys Ser Lys Thr Cys Gly Lys Gly
915 920 925

Tyr Lys Lys Arg Ser Leu Lys Cys Leu Ser His Asp Gly Gly Val Leu
930 935 940

Ser His Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Phe Ile Asp
945 950 955 960

Phe Cys Thr Met Ala Glu Cys Ser
965

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